

SEQUENCE LISTING

AP20 Rec'd PCT/PTO 16 DEC 2005

<110> Advanced Technologies (Cambridge) Ltd

<120> Plant Limit Dextrinase Inhibitor

<130> RD-ATC-32

<140>

<141>

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 517

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (14) .. (457)

<400> 1

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1 5 10	

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Ala Val Leu Leu Ser Val Leu Ala Val Ala Ala Thr Leu Glu Ser	
15 20 25	

gtc aag gac gag tgc caa cca ggg gtg gac ttc ccg cat aac ccg tta	145
Val Lys Asp Glu Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu	
30 35 40	

gcc acc tgc cac acc tac gtg ata aaa cgg gtc tgc ggc cgc ggt ccc	193,
Ala Thr Cys His Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro	
45 50 55 60	

agc cgg ccc atg ctg gtg aag gag cgg tgc tgc ccg gag ctg gcg gcc	241
Ser Arg Pro Met Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala	
65 70 75	

gtc ccg gat cac tgc cgg tgc gag gcg ctg cgc atc ctc atg gac ggg	289
Val Pro Asp His Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly	
80 85 90	

gtg cgc acg ccg gag ggc cgc gtg gtt gag gga cgg ctc ggt gac agg	337
Val Arg Thr Pro Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg	
95 100 105	

cgt gac tgc ccg agg gag cag agg gcg ttc gcc gcc acg ctt gtc	385
Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val	
110 115 120	

acg gcg gcg gag tgc aac cta tcg tcc gtc cag gag ccg gga gta cgc	433
Thr Ala Ala Glu Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg	
125 130 135 140	

ttg gtg cta ctg gca gat gga tga cgatcgaaat gcgccaaagggt aatgaagcgg 487.
 Leu Val Leu Leu Ala Asp Gly
 145

agtactgtat acagaataaa agtactcgag 517

<210> 2
 <211> 147
 <212> PRT
 <213> Hordeum vulgare

<400> 2
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 1 5 10 15
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
 20 25 30
 Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
 35 40 45
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
 50 55 60
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
 65 70 75 80
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
 85 90 95
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
 100 105 110
 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
 115 120 125
 Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg Leu Val Leu Leu
 130 135 140
 Ala Asp Gly
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<210> 3
 <211> 672
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (39)...(482)

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 Met Ala Ser Asp His Arg
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 Arg Phe Val Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala Val Ala
 10 15 20

gcc gcc acc ttg gag agc gtc aag gac gag tgc caa cta ggg gtg gac 152
 Ala Ala Thr Leu Glu Ser Val Lys Asp Glu Cys Gln Leu Gly Val Asp
 25 30 35

ttc ccg cat aac ccg tta gcc acc tgc cac acc tac gtg ata aaa cgg 200
 Phe Pro His Asn Pro Leu Ala Thr Cys His Thr Tyr Val Ile Lys Arg
 40 45 50

gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg tgc 248
 Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg Cys
 55 60 65 70

 tgc cgg gag ctg gcg gcc gtc ccg gat cac tgc cgg tgc gag gcg ctg 296
 Cys Arg Glu Leu Ala Ala Val Pro Asp His Cys Arg Cys Glu Ala Leu
 75 80 85

 cgc atc ctc atg gac ggg gtg cgc acg ccg gag ggc cgc gtg gtt gag 344
 Arg Ile Leu Met Asp Gly Val Arg Thr Pro Glu Gly Arg Val Val Glu
 90 95 100

 gga cgg ctc ggt gac agg cgt gac tgc ccg agg gag gag cag agg gcg 392
 Gly Arg Leu Gly Asp Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala
 105 110 115

 ttc gcc gcc acg ctt gtc acg gcg gcg gag tgc aac cta tcg tcc gtc 440
 Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Ser Ser Val
 120 125 130

 cag gcg ccg gga gta cgc ttg gtg cta ctg gca gat gga tga 482
 Gln Ala Pro Gly Val Arg Leu Val Leu Ala Asp Gly
 135 140 145

 cgatgcaaat ggcgcaggat aatgaagcgg agtactgtat acagaataaa agtactcgag 542
 taaaaacaaa ctcataaata aacccttgta gatgtatgcg tatgtatctat ggtgtggaca 602
 gttaaattgt ggccgattga tgaataaaaaa aggttggAAC aaattaaatt gttgtgggtt 662
 catatactat 672

<210> 4
 <211> 147
 <212> PRT
 <213> Hordeum vulgare

<400> 4
 Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu
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 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
 20 25 30
 Cys Gln Leu Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
 35 40 45
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
 50 55 60
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
 65 70 75 80
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
 85 90 95
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
 100 105 110
 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
 115 120 125
 Cys Asn Leu Ser Ser Val Gln Ala Pro Gly Val Arg Leu Val Leu Leu
 130 135 140
 Ala Asp Gly
 145

<210> 5
 <211> 621
 <212> DNA
 <213> *Triticum aestivum*

<220>
 <221> CDS
 <222> (45)..(506)

<400> 5
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 Met Ala Ser Asn
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cat cgt cgc ttc ctc tcc ggc gcc gtc ttg ctc tca gtc ctc gcc 104
 His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala
 5 10 15 20

gcc gtg gcc gcc ctg gag agc gtt gag gac gag tgc cag cca ggg gtg 152
 Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys Gln Pro Gly Val
 25 30 35

gcc ttc ccg cac aac gca tta gcc acc tgc cac acc tac gtg atc aaa 200
 Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr Tyr Val Ile Lys
 40 45 50

cgg gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg 248
 Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg
 55 60 65

tgt tgc cgg gag ctg gcg gtc ccg gat tac tgc cgg tgc gag gca 296
 Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys Arg Cys Glu Ala
 70 75 80

ctg cgc gtc ctc atg gat ggg gtg cgc gcg gag gag ggc cac gtg gtg 344
 Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu Gly His Val Val
 85 90 95 100

gag ggc cgc ctt ggt gac aga cgt gac tgc ccg agg gag gcg cag cgg 392
 Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Ala Gln Arg
 105 110 115

gag ttc gcc gcc acg ctg acg gcg gcg gag tgc aac ctg ccg acc 440
 Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Pro Thr
 120 125 130

gtc tcg gga gtc ggg agt aca ctt ggt gcg acc ggc aga tgg atg acg 488
 Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly Arg Trp Met Thr
 135 140 145

atc gaa ttg ccc aag taa tgaagcgatc aaggcaagta ctctactggc 536
 Ile Glu Leu Pro Lys
 150

agatggagta ctgcgtatgt aataaaaagta ctcaagtgaa aacaaataaa taaagcttgt 596

gagctgtatg cgtatgaaaa aaaaa 621

<210> 6
 <211> 153
 <212> PRT
 <213> Triticum aestivum

<400> 6

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Ser	Val	Leu	Ala	Ala	Val	Ala	Ala	Leu	Glu	Ser	Val	Glu	Asp	Glu	Cys
					20				25						30
Gln	Pro	Gly	Val	Ala	Phe	Pro	His	Asn	Ala	Leu	Ala	Thr	Cys	His	Thr
					35				40						45
Tyr	Val	Ile	Lys	Arg	Val	Cys	Gly	Arg	Gly	Pro	Ser	Arg	Pro	Met	Leu
					50				55						60
Val	Lys	Glu	Arg	Cys	Cys	Arg	Glu	Leu	Ala	Val	Val	Pro	Asp	Tyr	Cys
					65				70						80
Arg	Cys	Glu	Ala	Leu	Arg	Val	Leu	Met	Asp	Gly	Val	Arg	Ala	Glu	Glu
					85				90						95
Gly	His	Val	Val	Glu	Gly	Arg	Leu	Gly	Asp	Arg	Asp	Cys	Pro	Arg	
					100				105						110
Glu	Ala	Gln	Arg	Glu	Phe	Ala	Ala	Thr	Leu	Val	Thr	Ala	Ala	Glu	Cys
					115				120						125
Asn	Leu	Pro	Thr	Val	Ser	Gly	Val	Gly	Ser	Thr	Leu	Gly	Ala	Thr	Gly
					130				135						140
Arg	Trp	Met	Thr	Ile	Glu	Leu	Pro	Lys							
					145				150						

<210> 7
 <211> 444
 <212> DNA

<213> Hordeum spontaneum

<220>
 <221> CDS
 <222> (1)..(444)

<400> 7

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1					5				10						15	
att	ctc	gcc	gcc	act	gtc	acc	agt	ttc	ggg	gat	atg	tgt	gtc	cca	ggg	96
Ile	Leu	Ala	Ala	Thr	Val	Thr	Ser	Phe	Gly	Asp	Met	Cys	Ala	Pro	Gly	
					20				25						30	
gat	gcg	ttg	cca	gcc	aac	cct	ctc	aga	gcc	tgc	cgc	acc	tat	gtg	gtt	144
Asp	Ala	Leu	Pro	Ala	Asn	Pro	Leu	Arg	Ala	Cys	Arg	Thr	Tyr	Val	Val	
					35				40						45	
agt	caa	atc	tgc	cat	gta	ggc	cct	aga	cta	tcc	acc	tgg	gac	atg	aag	192
Ser	Gln	Ile	Cys	His	Val	Gly	Pro	Arg	Leu	Ser	Thr	Trp	Asp	Met	Lys	
					50				55						60	
agg	cgg	tgc	tgc	gac	gag	ctg	tcg	gcc	atc	ccg	gcg	tac	tgc	aga	tgc	240
Arg	Arg	Cys	Cys	Asp	Glu	Leu	Ser	Ala	Ile	Pro	Ala	Tyr	Cys	Arg	Cys	
					65				70						80	

gag gcg ctg cgt atc atc atc gat ggg aca gta act tgg cag ggt gtg 288
 Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
 85 90 95

ttc ggt gcc tac ttc aag gac atg ccc aac tgc cct agg gtg atg caa 336
 Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
 100 105 110

acg agc tac gcc gcc aac ctc gtc aac cog cag gag tgc aac cta tgg 384
 Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
 115 120 125

act atc cac ggc agc ccg tcc tgc ccc gaa ctg cag ccc gga tat gaa 432
 Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
 130 135 140

gtg gtc ttg taa 444
 Val Val Leu
 145

<210> 8
 <211> 147
 <212> PRT
 <213> Hordeum spontaneum

<400> 8
 Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala
 1 5 10 15
 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
 20 25 30
 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
 35 40 45
 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
 50 55 60
 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
 65 70 75 80
 Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
 85 90 95
 Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
 100 105 110
 Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
 115 120 125
 Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
 130 135 140
 Val Val Leu
 145

<210> 9
 <211> 483
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1) .. (483)

<400> 9

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tcc gtg ctc gcg gcg acg gcg acc atg gcg gag tac cac cac caa gac	96
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp	
20 25 30	
cag gtg gtc tac acc ccg ggc ccg ctc tgt cag cca gga atg ggc tac	144
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr	
35 40 45	
ccg atg tac ccg ctc ccg cgt tgc ccg gcg ttg gtg aag cgc cag tgc	192
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys	
50 55 60	
gtc ggc cgt ggc acg gcc gcc gcc gag cag gtc ccg cga gac tgc	240
Val Gly Arg Gly Thr Ala Ala Ala Glu Gln Val Arg Arg Asp Cys	
65 70 75 80	
tgc ccg cag ctc gcc gcc gtc gac gac agc tgg tgc agg tgc gag gcg	288
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala	
85 90 95	
atc agc cac atg ctg gga ggc atc tac agg gag ctc ggc gcc ccc gat	336
Ile Ser His Met Leu Gly Gly Ile Tyr Arg Glu Leu Gly Ala Pro Asp	
100 105 110	
gtc ggg cac ccc atg tcc gag gtg ttc cgc ggc tgc ccg aga ggg gac	384
Val Gly His Pro Met Ser Glu Val Phe Arg Gly Cys Arg Arg Gly Asp	
115 120 125	
ttg gag cgc gcg gcg agc ctc ccg gcg ttc tgc aac gtg gac atc	432
Leu Glu Arg Ala Ala Ser Leu Pro Ala Phe Cys Asn Val Asp Ile	
130 135 140	
ccc aac ggc gga ggt ggt gtc tgc tac tgg ctg gcg aga tct ggc tac	480
Pro Asn Gly Gly Val Cys Tyr Trp Leu Ala Arg Ser Gly Tyr	
145 150 155 160	

tag

483

<210> 10
<211> 160
<212> PRT
<213> Oryza sativa

<400> 10
Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Ala Val Val
1 5 10 15
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60
Val Gly Arg Gly Thr Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala

85	90	95
Ile Ser His Met Leu Gly Gly Ile Tyr Arg Glu Leu Gly Ala Pro Asp		
100	105	110
Val Gly His Pro Met Ser Glu Val Phe Arg Gly Cys Arg Arg Gly Asp		
115	120	125
Leu Glu Arg Ala Ala Ala Ser Leu Pro Ala Phe Cys Asn Val Asp Ile		
130	135	140
Pro Asn Gly Gly Gly Val Cys Tyr Trp Leu Ala Arg Ser Gly Tyr		
145	150	155
		160

<210> 11
<211> 707
<212> DNA
<213> Triticum durum

<220>
<221> CDS
<222> (27) .. (533)

<400> 11
agcgaaccag acttggttag aatacc atg gcg tgc aag tcc agc tgc agc ctc 53
Met Ala Cys Lys Ser Ser Cys Ser Leu
1 5

ctc ctc ttg gcc gcc gtc ctg ctc tcc gtc ttg gcc gct gct tcc gcc 101
Leu Leu Leu Ala Ala Val Leu Leu Ser Val Leu Ala Ala Ala Ser Ala
10 15 20 25

tcc ggc agc tgc gtc cca ggg gtg gct ttt cgg acc aat ctt ctg cca 149
Ser Gly Ser Cys Val Pro Gly Val Ala Phe Arg Thr Asn Leu Leu Pro
30 35 40

cac tgc cgc gac tat gtg tta caa caa act tgc ggc acc ttc acc cct 197
His Cys Arg Asp Tyr Val Leu Gln Gln Thr Cys Gly Thr Phe Thr Pro
45 50 55

ggg tca aag tta ccc gaa tgg atg aca tct gcg tcg ata tac tcc cct 245
Gly Ser Lys Leu Pro Glu Trp Met Thr Ser Ala Ser Ile Tyr Ser Pro
60 65 70

ggg aaa ccg tac ctc gcc aag ttg tat tgc tgc cag gag ctc gca gaa 293
Gly Lys Pro Tyr Leu Ala Lys Leu Tyr Cys Cys Gln Glu Leu Ala Glu
75 80 85

att tct cag cag tgc cgg tgc gag gcg ctg cgc tac ttc ata gcg ttg 341
Ile Ser Gln Gln Cys Arg Cys Glu Ala Leu Arg Tyr Phe Ile Ala Leu
90 95 100 105

ccg gta ccg tct cag cct gtg gac ccg agg tcc ggc aat gtt ggt gag 389
Pro Val Pro Ser Gln Pro Val Asp Pro Arg Ser Gly Asn Val Gly Glu
110 115 120

agc ggc ctc atc gat ctg ccc gga tgc ccc agg gag atg caa tgg gac 437
Ser Gly Leu Ile Asp Leu Pro Gly Cys Pro Arg Glu Met Gln Trp Asp
125 130 135

ttc gtc aga tta ctc gtc gcc ccg ggg cag tgc aac ttg gcg acc att 485
Phe Val Arg Leu Leu Val Ala Pro Gly Gln Cys Asn Leu Ala Thr Ile
140 145 150

cac aat gtt cga tac tgc ccc gcc gtc gaa cag cct ctg tgg atc tag 533
 His Asn Val Arg Tyr Cys Pro Ala Val Glu Gln Pro Leu Trp Ile
 155 160 165

agataaaaatc agtcgctcgt gaataagcat gcatgttgc a tccataggcg tgggtgtgc 593
 atgtatacat atgtgagctc cgccgcgtca acatgtgtgg gctatctgct atgaatgaga 653
 ataaaagagaa tcattctgtg gtttttaat ttcaactaaa aaaaaaaaaa aaaa 707

<210> 12
 <211> 168
 <212> PRT
 <213> Triticum durum

<400> 12
 Met Ala Cys Lys Ser Ser Cys Ser Leu Leu Leu Leu Ala Ala Val Leu
 1 5 10 15
 Leu Ser Val Leu Ala Ala Ser Ala Ser Gly Ser Cys Val Pro Gly
 20 25 30
 Val Ala Phe Arg Thr Asn Leu Leu Pro His Cys Arg Asp Tyr Val Leu
 35 40 45
 Gln Gln Thr Cys Gly Thr Phe Thr Pro Gly Ser Lys Leu Pro Glu Trp
 50 55 60
 Met Thr Ser Ala Ser Ile Tyr Ser Pro Gly Lys Pro Tyr Leu Ala Lys
 65 70 75 80
 Leu Tyr Cys Cys Gln Glu Leu Ala Glu Ile Ser Gln Gln Cys Arg Cys
 85 90 95
 Glu Ala Leu Arg Tyr Phe Ile Ala Leu Pro Val Pro Ser Gln Pro Val
 100 105 110
 Asp Pro Arg Ser Gly Asn Val Gly Glu Ser Gly Leu Ile Asp Leu Pro
 115 120 125
 Gly Cys Pro Arg Glu Met Gln Trp Asp Phe Val Arg Leu Leu Val Ala
 130 135 140
 Pro Gly Gln Cys Asn Leu Ala Thr Ile His Asn Val Arg Tyr Cys Pro
 145 150 155 160
 Ala Val Glu Gln Pro Leu Trp Ile
 165

<210> 13
 <211> 712
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (33)...(500)

<400> 13
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 Met Ala Ser Ser Ser Ser
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agc cac cgc cgc ctc atc ctc gca gcc gcc gtc ctg ctc tcc gtg ctc 101
 Ser His Arg Arg Leu Ile Leu Ala Ala Val Leu Leu Ser Val Leu
 10 15 20

gct gct gcc agc gcc agc ggg acc tcc tgc gtg ccg ggg tgg gcc 149
 Ala Ala Ala Ser Ala Ser Ala Gly Thr Ser Cys Val Pro Gly Trp Ala
 25 30 35

atc ccg cac aac ccg ctc ccg agc tgc ccg tgg tac gtg acc agc ccg 197
 Ile Pro His Asn Pro Leu Pro Ser Cys Arg Trp Tyr Val Thr Ser Arg
 40 45 50 55

acc tgc ggc atc ggg ccg ccg ctc ccg tgg ccg gag ctg aag agg aga 245
 Thr Cys Gly Ile Gly Pro Arg Leu Pro Trp Pro Glu Leu Lys Arg Arg
 60 65 70

tgc tgc ccg gag ctg gcg gac atc ccg gcg tac tgc ccg acg gcg 293
 Cys Cys Arg Glu Leu Ala Asp Ile Pro Ala Tyr Cys Arg Cys Thr Ala
 75 80 85

ctg agc atc ctc atg gac ggc gcg atc ccg cct ggc ccg gac gcg cag 341
 Leu Ser Ile Leu Met Asp Gly Ala Ile Pro Pro Gly Pro Asp Ala Gln
 90 95 100

ctg gag ggc ccg cta gag gac ctg ccg ggc tgc ccg ccg gag gtg cag 389
 Leu Glu Gly Arg Leu Glu Asp Leu Pro Gly Cys Pro Arg Glu Val Gln
 105 110 115

agg gga ttc gcc acc ctc gtc acg gag gcc gag tgc aac ctg gcc 437
 Arg Gly Phe Ala Ala Thr Leu Val Thr Glu Ala Glu Cys Asn Leu Ala
 120 125 130 135

acc atc agc ggc gtc gcc gaa tgc ccc tgg att ctc ggc ggc gga acg 485

Thr Ile Ser Gly Val Ala Glu Cys Pro Trp Ile Leu Gly Gly Thr
 140 145 150

atg ccc tcc aag taa ctgcgaagag catagtgcata gaggaaatgag cttgttagcta 540
 Met Pro Ser Lys
 155

gctcatatgt ctgaataata agcacagcaa gaagatgaat gcatttctcg gatcggtcat 600

ccgaaacaat aattaaaggg gatccggatt tgttcttgc atataattaa cgattcctgt 660

tataacttggg agtagctagg ctcgtcccca tccaatgc当地 gaaaaaaaaaa aa 712

<210> 14
 <211> 155
 <212> PRT
 <213> Zea mays

<400> 14
 Met Ala Ser Ser Ser Ser His Arg Arg Leu Ile Leu Ala Ala
 1 5 10 15
 Ala Val Leu Leu Ser Val Leu Ala Ala Ala Ser Ala Ser Ala Gly Thr
 20 25 30
 Ser Cys Val Pro Gly Trp Ala Ile Pro His Asn Pro Leu Pro Ser Cys
 35 40 45
 Arg Trp Tyr Val Thr Ser Arg Thr Cys Gly Ile Gly Pro Arg Leu Pro
 50 55 60
 Trp Pro Glu Leu Lys Arg Arg Cys Cys Arg Glu Leu Ala Asp Ile Pro
 65 70 75 80

Ala Tyr Cys Arg Cys Thr Ala Leu Ser Ile Leu Met Asp Gly Ala Ile
 85 90 95
 Pro Pro Gly Pro Asp Ala Gln Leu Glu Gly Arg Leu Glu Asp Leu Pro
 100 105 110
 Gly Cys Pro Arg Glu Val Gln Arg Gly Phe Ala Ala Thr Leu Val Thr
 115 120 125
 Glu Ala Glu Cys Asn Leu Ala Thr Ile Ser Gly Val Ala Glu Cys Pro
 130 135 140
 Trp Ile Leu Gly Gly Thr Met Pro Ser Lys
 145 150 155

<210> 15
 <211> 122
 <212> PRT
 <213> Eleusine coracana

<400> 15
 Ser Val Gly Thr Ser Cys Ile Pro Gly Met Ala Ile Pro His Asn Pro
 1 5 10 15

Leu Asp Ser Cys Arg Trp Tyr Val Ala Lys Arg Ala Cys Gly Val Gly
 20 25 30

Pro Arg Leu Ala Thr Gln Glu Met Lys Ala Arg Cys Cys Arg Gln Leu
 35 40 45

Glu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Val Arg Ile Leu Met
 50 55 60

Asp Gly Val Val Thr Pro Ser Gly Gln His Glu Gly Arg Leu Leu Gln
 65 70 75 80

Asp Leu Pro Gly Cys Pro Arg Gln Val Gln Arg Ala Phe Ala Pro Lys
 85 90 95

Leu Val Thr Glu Val Glu Cys Asn Leu Ala Thr Ile His Gly Gly Pro
 100 105 110

Phe Cys Leu Ser Leu Leu Gly Ala Gly Glu
 115 120

<210> 16
 <211> 121
 <212> PRT
 <213> Secale cereale

<400> 16
 Ser Val Gly Gly Gln Cys Val Pro Gly Leu Ala Met Pro His Asn Pro
 1 5 10 15

Leu Gly Ala Cys Arg Thr Tyr Val Val Ser Gln Ile Cys His Val Gly
 20 25 30

Pro Arg Leu Phe Thr Trp Asp Met Lys Arg Arg Cys Cys Asp Glu Leu
 35 40 45

Leu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Leu Arg Ile Leu Met
 50 55 60

Asp Gly Val Val Thr Gln Gln Gly Val Phe Glu Gly Gly Tyr Leu Lys
65 70 75 80

Asp Met Pro Asn Cys Pro Arg Val Thr Gln Arg Ser Tyr Ala Ala Thr
85 90 95

Leu Val Ala Pro Gln Glu Cys Asn Leu Pro Thr Ile His Gly Ser Pro
100 105 110

Tyr Cys Pro Thr Leu Gln Ala Gly Tyr
115 120

<210> 17

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 17

accaataaac tagtatcaac aatggcatcc gacca

35

<210> 18

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 18

ccaaacctttt ttattcatca atcggccaca

30

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 19

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27

<210> 20

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 20

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29

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<220>
<223> Description of Artificial Sequence: PCR primer

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23

<210> 22
<211> 24
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<220>
<223> Description of Artificial Sequence: PCR primer

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24

<210> 23
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<400> 23
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22

<210> 24
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20

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<211> 20
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<223> Description of Artificial Sequence: PCR primer

<400> 25
ccatgccttag ggtcacactt

20